

Run on: August 21, 2001, 12:07:03 ; Search time 22.69 Seconds
 (without alignments)
 1830.929 Million cell updates/sec

Title: US-09-486-334-2
 Perfect score: 1601
 Sequence: 1 MATC'DTCRGNTQDDDSRF. IPCLTMDQTSYLTENSDIVI 314

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTRIMBL_16:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rhodent:
 12: sp_unclassified:
 13: sp_vertebrate:
 14: sp_virus:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result NO.	Score	Query Match Length	DB ID	Description
1	1541	100.0	314	043297
2	1611	98.2	314	10 043297
3	1215	74.0	391	042588
4	1208	73.6	336	10 042532
5	877	53.4	347	10 P93544
6	872	53.1	289	10 Q9MAZ3
7	869	53.0	294	10 Q9JP53
8	861	52.5	289	10 Q9SDP2
9	849.5	51.8	312	10 042538
10	711	43.3	323	10 Q9PZJ4
11	711	43.3	368	10 O9STB0
12	699	42.6	315	10 Q9SEV6
13	647.5	39.6	272	2 Q9JR86
14	647.5	39.5	273	2 Q9KNT2
15	628.5	38.4	402	10 Q9SLZ8
16	610.5	37.2	312	10 Q9L3R1
17	587.5	35.8	299	10 O81795
18	472.5	28.8	270	3 Q9US33
19	25.7	22.7	2 032919	mvrhah+ari

ALIGNMENTS

RESULT	1
043297	PRELIMINARY;
043297	PRT; 314 AA.
DT	01-NOV-1996 (TRIMBLE1, 01, created)
DT	01-NOV-1996 (TRIMBLE1, 01, last sequence update)
DE	01-OCT-2000 (TRIMBLE1, 15, Last annotation update)
DE	SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
DE	(FL4J16.18)
OS	Arabidopsis thaliana (Mouse-ear cress)
OC	Bukarvota; Virdiplante; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC	Brasicales; Brassicaceae; Arabidopsis.
RN	[1] NCBI-TaxID=3702;
RP	SEQUENCE FROM N.A.
RC	STRAIN=COLUMBIA;
RX	MEDLINE=9515433; PubMed=7851429;
RA	Ruffet M.L., Lebrun M., Droux M., Douce R.;
RT	"Subcellular distribution of serine acetyltransferase from Pisum sativum and characterization of an Arabidopsis thaliana putative cytosolic isoform";
RT	J. Biochem. 227:500-509(1995).
RN	[2] Ruffet M.L., Lebrun M., Droux M., Douce R.;
RP	SEQUENCE FROM N.A.
RA	Ruffet M.L., Lebrun M., Droux M., Douce R.;
RA	Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN	[3] RUFFET M.L., LEBRUN M., DROUX M., DOUCE R.;
RP	SEQUENCE FROM N.A.
RA	Shinn P., Brooks P., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altaf H., Bei Q., Chin C., Chiuou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Hawing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham T., Sakano H., Schwartz J., Southwick A., Thaveri A., Tohiumi M., Vajenberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.; Federici N.A., Theologis A.,
RT	"Genomic sequence for Arabidopsis thaliana BAC FL4J16 from chromosome I";
RT	Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN	[4]

Tue Aug 21 12:47:49 2001

DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE).
 OS Arabidopsis thaliana (Mouse-ear cress). Spermatophyta;
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Magnoliophyta; eudicots; Rosidae; eurosids II;
 OC Brassicaceae; Brassicidae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.; Submitted (AUG-1997) to the EMBL/GenBank/DDJB databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.; Submitted (MAY-2000) to the EMBL/GenBank/DDJB databases.
 RL [7]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.; Submitted (MAY-2000) to the EMBL/GenBank/DDJB databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Conn S., Kim C., Altafi H., Bei B., Chin C., Chou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Schwartz J., Southwick A.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveria A., Toriumi M., Vayberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDJB databases.
 RL -!- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 DR EMBL: L424212; AAC27474-1; -.
 DR Mendl; 6700; Arath; 1221; 6700.
 DR InterPro; IPR014551; -.
 DR Pfam; PF00132; hexapep; 3.
 DR PROSITE; PS0001; HEXAEP_TRANSFERASES; 1.
 DR KW PROSITE; PS0001; HEXAEP_TRANSFERASE; 1.
 DR Transferase; Acetyltransferase.
 KW SQ Sequence 314 AA; 34259 MW; A096DF6D2768E21C CRC64;

Query Match 98.2%; Score 1611; DB 10; Length 314;
 Best Local Similarity 98.1%; Pred. No. 6..9e-123; Indels 0; Gaps 0;
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACCIDTGTGNQDDDSRFCCIKNFRPGFSVWKHHTQIEDDDWIKMLPEAKSDV 60
 1 MATCIDIICRTGNQDDDSRFCCIKNFRPGFSVNRKTHHTQIEDDDWIKMLPEAKSDV 60

Db 61 KQEPILSNYYASITSHRSLESALAHILSVKLNSLNLPNTLEFLISWLESEPIEST 120
 61 KOEPLISNNYYASITSHRSLESALAHILSVKLNSLNLPNTLEFLISWLESEPIEST 120

QY 121 KQDLIAKVERDPACTSYVHCPFLGKGFLACQAHRAHTLWKQNRTVALLIONRVESEA 180
 121 KQDLIAKVERDPACTSYVHCPFLGKGFLACQAHRAHTLWKQNRTVALLIONRVESEA 180

QY 181 VDHPGAKTGKIGLILDHATGVVGETAVGDNNTILHGVTLGTTGKQSGDRHKPDKGDVL 240
 181 VDHPGAKTGKIGLILDHATGVVGETAVGDNNTILHGVTLGTTGKQSGDRHKPDKGDVL 240

Db 241 IGAGSCILGNITIGEGAKGSVWVVDKPARTAVGNPARLIGGKENPRKHDKIPCLTM 300
 241 IGAGSCILGNITIGEGAKGSVWVVDKPARTAVGNPARLIGGKENPRKHDKIPCLTM 300

QY 301 DQTSVLTENSDYVI 314
 301 DQTSVLTENSDYVI 314

Db 301 DQTSVLTENSDYVI 314

RESULT 3
 Q2532 PRELIMINARY; PRT; 391 AA.

ID Q42532
 AC 042532; 043740; 043739;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE).
 DE (SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SATI PRECURSOR).
 GN SAV-1 OR SATA OR SAT A.
 OS Arabidopsis thaliana (Mouse-ear cress). Spermatophyta;
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Magnoliophyta; eudicots; Rosidae; eurosids II;
 OC Brassicaceae; Brassicidae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE-96270381; PubMed=6639741;
 RA Roberts M.A., Wray J.L.;
 DT "Cloning and characterization of an Arabidopsis thaliana cDNA clone
 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

RESULT 2
 Q42508 PRELIMINARY; PRT; 314 AA.

RL	Plant. Mol. Biol.	30:1041-1049(1996).	PRT;	336 AA.
RN	[2]			
RP	SEQUENCE OF 80-391 FROM N.A.-			
RC	STRAIN=CV; COUNTRY; TISSUE=LEAF;			
RX	MEDLINE=93121457; PubMed=7821427;			
RA	Bogdanova N., Bork C., Hell R.;			
RT	"Cysteine biosynthesis in plants: isolation and functional identification of a cDNA encoding a serine acetyltransferase from Arabidopsis thaliana.";			
RT	FEBs Lett.	358:43-47(1995).		
RN	[3]			
RP	SEQUENCE OF 56-391 FROM N.A.			
RC	STRAIN=CV; COUNTRY; TISSUE=LEAF;			
RA	Hall R., Bogdanova N.;			
RL	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RA	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RX	Pubmed=10907853;			
RA	Nakamura Y.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,605 bp covered by ninety <i>Pl</i> , TAC and BAC clones.";			
RT	DNA Res. 7:217-221(2000)			
CC	-.- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-SERINE			
DR	EMBL: U22954; AAC07778_1; -.			
DR	EMBL: X82888; CAAS8061_1; -.			
DR	EMBL: X80938; CAA6913_1; -.			
DR	EMBL: AP000375; BAB0102_1; -.			
DR	Mendel; 6698; Arath;1221;6698.			
DR	InterPro; IPR001451; -.			
DR	Pfam; PF00132; hexapep; 3.			
DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.			
DR	KW Transferease; Acetyltransferase; 1.			
SQ	SEQUENCE 391-AA; 42720 MW; A3BD09DEA53C10E2 CRC64;			
Query	Match	74.0%; Score 1215; DB 10; Length 391;		
Best	Local Similarity	72.0%; Pred. No. 1; e=90;		
Matches	242; Conservative	71.7%; Pred. No. 3; e=90;		
4;	Mismatches	31; Mismatches		
QY	1 MATCIDCTRGTGNTQ-----DDDSRCCIKNFRRPGS---VNRKIHHTQ--IED			
Db	1 MACIDCTRGTGPKQIISPRDSSKKHDDESGRMMVFRYDPRSSFNGTQTKLHLRPLLED			
QY	45 -----DDDWIKMELEEKADSKWQKEPILSNYVYASITSHRSLESALAHITSYVKSUNLNLP			
Db	61 LDRDAEFDWDWAKIREAKSDIAKEDIPATPVSYAVHASYIVSQRSLRPAALANTLSVKSUNLNLP			
QY	99 SNTLFELPFISVLEESPETIESTKQDLIAVKEKRPACISVYHCPFGKGFLCAOHRIATH			
QY	56 MACIDCTRGTGPKQIISPRDSSKKHDDESGRMMVFRYDPRSSFNGTQTKLHLRPLLED			
Db	121 SNTLFDFLFSGGLOGNPDVIESVKDVLAYKERPDACTSYVHCFLFHKGFLCAOHRIATH			
QY	159 LAKQNKRKVALLIONVRSSEFAVDIHPGAXIGKGILLDHATGWIGETAWVGDNVTHG			
Db	181 LWTQDKRKTIALLJQNRSEAFAVDFHPGAKIGTGILLDHATGWIGETAWVGDNVTHG			
QY	219 VTLGGTQKOSGRHPKGIGVGLIGAGSCITGNITIGEGAKIGGSVWVNVKDPARTAVGN			
Db	241 VTLGGTQKOSGRHPKGIGVGLIGACTCGITGNITIGEGAKIGAGSVWVLDVPTERTAVGN			
Db	301 PARLIGGKDNPKTHDKIPLGLMDOTSHISENSDYVI 336			
RESULT	5			
P93544	PRELIMINARY;	PRT;	347 AA.	
ID	P93544			
AC	P93544;			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DT	01-OCT-2000 (TREMBLrel. 03, Last sequence update)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DR	DR SERINE ACETYLTRANSFERASE.			
OS	Spinacia olaracea (Spinach).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.			
OC	NCBI TaxID=3562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PARADE; TISSUE=LEAVES;			
RA	Saito K., Takagi Y.;			
RL	Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.			

DR	EMBL; DR8530; BA113635.1; -.	QY	164 RKIVALLIONRVSSEFAVDIHPGAKIGKGCILDHATGVIGETAWGDNVSLHGYLGG 223
DR	EMBL; DR8529; BA113634.1; -.	Db	139 RPLALHSRVADLSDVPHARIGKGILDHATGVIGETAVIGNNVSLHRYLGG 198
Mendel;	10792; Spelol; 1221; 10792.	QY	224 TKGOSDRHKIGDVLIGAGSCLIGNTIGEAKIGSGSVVKDPARTAVGNPARI 283
DR	InterPro; IPR001451; -.	Db	199 TKGAGDRHPKIGGVLIGAGATLIGNRIGAKIGAGKAGSVVLLDVPPRTAVGNPARI 258
DR	PROSITE; PS00101; HEXAPEPTRANSFERASES; 1.	QY	284 GGKEMPKRHKIPCLMDOTSYLEWSYVI 314
KW	Transferase.	Db	259 GGKEPKSMEDVCEMSMTFISEWSDII 289
SEQUENCE	347 AA; 37256 MW; FBAB365488DB6B0E CRC64;	RESULT	7
Query Match	53.4%; Score 877; DB 10; Length 347;	QY	039533 PRELIMINARY; PRT; 294 AA.
Best Local Similarity	56.6%; Pred. No. 2.9e-63;	ID	039533 PRELIMINARY; PRT; 294 AA.
Matches	163; Conservative 53; Mismatches 70; Indels 2; Gaps 1;	AC	039533 PRELIMINARY; PRT; 294 AA.
OY	29 PG-FSVNRRIKHTQEDDDVVWVRLERAKSKDVKQEPILTSNYYASITSHRSLESALAH 86	DT	01-NOV-1996 (TREMBLR. 01, Created)
Db	60 PGGDLSVAPSVGHJANNELAWLQWQIKGEARRDADSEPALASYLSTLSSLSLSLF 119	DT	01-MAR-2001 (TREMBLR. 01, Last sequence update)
OY	87 ILISVKNLNPWLPFLFISVLEESPEIESTSKDQDIAVVERDPACISTVHCGFKFGK 146	DE	SERINE ACETYLTRANSFERASE.
Db	120 HLGNRKLCSSTLSTLSDYDFLNLTSLSLSDSLLAVADLAARVRDPACVSFHCCLNYK 179	GN	SAT.
OY	147 FLAGQAHRTAHTWVKKRKIVALLIQNRYSEFAVDIHPGAKIGKGILDHATGVIGET 206	OS	Citrullus lanatus (watermelon) (<i>Citrullus vulgaris</i>).
Db	180 FLAQSHRTIAHKWQNDRPLAALHRSRISDVFAVQIHPAARIKGKIGLFDHATGVIGET 239	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OY	207 AVVGDNVVILHGSVTLGGKGOKGDHRHKIGCIGVLLGASCCLIGNTTIGEAKIGSGSVVY 266	OC	Magnoliophyta; eudicots; Rosidae; eurosids I;
Db	240 AIGGNCISLHLHVTLGGKGAKGRHPKVGDVGLIGATLIGNRIGAKIGAGSVVL 299	OX	Cucurbitales; Cucurbitaceae; Citrullus.
OY	267 KDVPARTAVGVPARLIGGKENPRAKIDLTQPTISLYEWSPYI 314	[1]	SEQUENCE FROM N.A.
Db	300 IDVPPRPTAVGVPARLIGGKERPSQNSDVGESMDHTSFISEWSDII 347	RP	STRAIN=KINRO;
RESULT	6	RC	Saito K., Inoue K., Fukushima R., Noji M.,
Q8MAZ3	PRELIMINARY; PRT; 289 AA.	RA	RN submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
ID	Q8MAZ3; 01-OCT-2000 (TREMBLR. 15, Created)	RC	[2]
DT	01-OCT-2000 (TREMBLR. 15, Last sequence update)	RA	SEQUENCE FROM N.A.
DT	01-MAR-2001 (TREMBLR. 16, Last annotation update)	RC	STRAIN=KINRO; TISSUE=GREEN LEAVES;
DE	SERINE ACETYLTRANSFERASE.	RA	MEDLINE=9532343; PubMed=7608200;
GN	ASRT5.	RT	Saito K., Yokoyama H., Noji M., Murakoshi I.;
OS	Allium tuberosum.	RT	Molecular cloning and characterization of a plant serine acetyltransferase playing a regulatory role in cysteine biosynthesis from watermelon.
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	RL	J. Biol. Chem. 270:16321-16326(1995).
OC	Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.	RN	[3]
OX	NCBI_TAXID=4683;	RP	SEQUENCE FROM N.A.
RN	[1]	RC	STRAIN=KINRO;
RP	SEQUENCE FROM N.A.	RA	Noji M., Inoue K., Saito K.,
RA	Urano Y., Saito K.,	RT	Submitted (Aug-1997) to the EMBL/GenBank/DDBJ databases.
RT	"Allium tuberosum" mRNA for serine acetyltransferase.;	DR	EMBL; DR5624; BA112843.1; -.
RT	Submitted (Mar-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; DA9535; BAQ08479.1; -.
DR	EMBL; AB04502; BAQ93000.1; -.	DR	EMBL; AB006530; BA21827.1; -.
DR	InterPro; IPR001451; -.	DR	Mendel; 7748; Cital; 1221; 7748.
DR	InterPro; IPR001451; -.	DR	InterPro; IPR001451; -.
DR	Pfam; PF00132; hexapep; 3.	DR	Pfam; PF00132; hexapep; 3.
DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.	DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
KW	TRANSFERASE.	DR	PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
SEQUENCE	289 AA; 30671 MW; 6DC2D784D25CF383 CRC64;	SQ	SEQUENCE FROM N.A.
Query Match	53.1%; Score 872; DB 10; Length 289;	QY	37 IHHTQEDDDVVWVRLERAKSKDVKQEPILTSNYYASITSHRSLESALAHLSVLSLN 96
Best Local Similarity	56.1%; Pred. No. 5.7e-63;	Db	17 VESTINNDTEWLWQIKAKARRDADSEPALASYLSTLSSLSLSFHGNKLCST 76
Matches	166; Conservative 43; Mismatches 62; Indels 0; Gaps 0;	QY	97 LPNTLLEFLFISVLEESPEIESTSKDQDIAVVERDPACISTVHCGFKFLACOHRIA 156
OY	44 DDDDWIKMELEEKSKVQEPILTSNYYASITSHRSLESALAHLSVLSLNLPSTWLF 103	Db	77 LLSTLTYDIFLNFASTDYCLRSAWADLQAAERDPACVSFHCCLNYKFLACOHRIA 156
Db	19 DESWWNIQKKEARRAESPARASLYSPILSRSLSFLANKLCSSTLSSLY 78	QY	157 HTLWKONRKIVALLIQNRYSEFAVDIHPGAKIGKGILDHATGVIGETAWGDNVSL 216
OY	104 ELFISVLEESPEIESTSKDQDIAVVERDPACISTVHCGFKFLACOHRIA 163	Db	137 HKLWNQRSPRLALOSRLADWFAVQIHPAARIKGKIGLFDHATGVVGETAVIGNVSL 196
Db	79 DLFLNALSTPFTILSATVADLIARRHDPACIGFSHCLNFKGFLAVOTIAHVLWSQS 138		

RESULT	8
Q9SP2	PRELIMINARY;
ID Q9SP2; AC Q9SP2;	PRT; 289 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DE SERINE ACETYLTRANSFERASE.	
OS Allium cepa (Onion).	
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Aliaceae; Allium.	
OX NCBI_TaxID=4679;	
RN [1]	
RP SEQUENCE FROM N A.	
RC STRAIN=CV. PUKEKOHE LONG KEEPER; TISSUE=ROOT;	
RA Pither-Joyce M.D.; McCallum J.A.; Wray J.L.;	
RT "Isolation of a serine acetyltransferase cDNA clone from Allium cepa.", Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
RL DR EMBL; AF212156; AAC19000.1; -.	
DR InterPro; IPR001451; -.	
DR Pfam; PF00132; hexapep; 3.	
KW PROSITE; PS00101; HEXAEP_TRANSFERASES; 1.	
SEQUENCE 289 AA; 30574 MW; 9EA376C54DA0AF13 CRC64;	
Query Match Best Local Similarity 52.5%; Score 861; DB 10; Length 289; Matches 162; Conservative 46; Mismatches 63; Indels 0; Gaps 0;	
QY 44 DDDDWKIRMLKEAKSDYKQEPILSNYYASTSHRSLESALAHITSVKUSNLNPNTLF 103	
Db 19 DESWWWWQIKAHZHARKESEPLASLYSTLHSLSLSPHANKCSSTLTSIK 78	
QY 104 ELFISVLEESPELIESESTKQDILAVKERDPACISYVHCFGLKGFLACQHRIATLWKON 163	
Db 79 DLFLNTLSTFPVLSSAVDLAARRHDPAVGVSCHLNFKGFLAVQTQRHLVLSQS 138	
QY 164 RKVALLIONVSESESADVDPGAKIGKGILDHATGVVITGEAVVGNVSIHGVTLGG 223	
Db 139 RKLPLALHSHVADLSDVTHPAAIRGKGILLDATGVVIGETAVIGNVSLHHVTLGG 198	
QY 224 TCKQSDGRHPKIGDGLIGAGSCILGNITIGEAKIGSGSVVVKDVPARTAVGNPARLI 283	
Db 199 TCKAGGDRHPKIGDGVLIGAGATLGNITRIGAGKVGAGSVVVLIDVPERTAVGNPARLI 258	
QY 284 GGKEMPRKRHKIPCLMDOTSYTEWSDVI 314	
Db 259 GGKEKPSVHEDVPGESMDHTSFISEWSDYII 289	
RESULT 9	
Q42538 PRELIMINARY; PRT; 312 AA.	
Q42538; AC Q42538; DT 01-NOV-1996 (TREMBLrel. 01, Created)	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)	
(SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) SAT-52).	
Arbiddosis thalana (Mouse-ear cress). Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Eukaryota; Viridiplantae; Tracheophyta; Spermatophyta; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;	
RESULT 10	
Q9ZPT4 PRELIMINARY; PRT; 323 AA.	
ID Q9ZPT4 AC Q9ZPT4; DT 01-MAY-1999 (TREMBLrel. 10, Created)	
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).	
GN SAT-106.	
OS Arbiddosis thalana (Mouse-ear cress). Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;	
OC Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
OC NCBI_TaxID=3702;	
RN [1]	
RP SEQUENCE FROM N A.	
RC STRAIN=COLUMBIA;	
RA MEDLINE=9720105; PubMed=9048879;	
RA Howard J.R.; Roberts M.A.; Wray J.L.;	
RT "Cysteine biosynthesis in higher plants: a new member of the Arabidopsis thaliana serine acetyltransferase small gene-family obtained by functional complementation of an Escherichia coli cysteine auxotroph.", "Cysteine biosynthesis in higher plants: a new member of the Arabidopsis thaliana serine acetyltransferase small gene-family obtained by functional complementation of an Escherichia coli cysteine auxotroph.",	
RT Rl Biochim. Biophys. Acta 1350:123-127(1997).	
RN [2]	
RP SEQUENCE FROM N A.	
RC STRAIN=COLombIA;	
RA MEDLINE=9803884; PubMed=9734815;	
RA Kotani H.; Nakamura Y.; Sato S.; Asamizu E.; Kaneko T.; Miyajima N.; Tabata S.;	
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Physically assigned P1 and TAC clones.", "Structural analysis of Arabidopsis thaliana chromosome 5. VII. Physically assigned P1 and TAC clones.",	
RT RL DNA Res. 5:205-216(1998).	
DR EMBL; U03298; AAC46555.1; -.	
DR DR EMBL; AB013392; BAB09894.1; -.	
DR Mendel; 6699; Arati;1221;6699.	
DR DR InterPro; IPR001451; -.	
DR PRAM; PF00132; hexapep; 3.	
KW PROSITE; PS00101; HEXAEP_TRANSFERASES; 1.	
DR Transferase; Acetyltransferase.	
SQ SEQUENCE 312 AA; 32770 MW; 15835510FF314A08 CRC64;	
Query Match Best Local Similarity 51.8%; Score 849.5; DB 10; Length 312; Matches 160; Conservative 45; Mismatches 62; Indels 1; Gaps 0;	
QY 48 VWTKMLEAKSKDQEVTLNSYYASITSHRSLESALAHITSVKUSNLNPNTLFELI 107	
Db 45 LWIQKIAEARRDAEAPEALASYLSTLHSLSLSPHANKCSSTLTSIK 104	
QY 108 SYLEESTEELESTKQDILAVKERDPACISVHCFGLKGFLACQHRIATLWKON 167	
Db 105 NTFSDDPSLRNATVADIRRARRVDRDPACISPSHCLNKFQFLAQHRYVSKLMTOSRKL 164	
QY 168 ALIQLQNVSESFADVDPGAKIGKGILDHATGVVITGEAVVGDVNSVLLHGVTGCGKQ 227	
Db 165 ALAHLHSIDFADVDPGAKIGKGILDHATGVVITGEAVVGDVNSVLLHGVTGCGKQ 227	
QY 228 SGDRHKIGDGVLIGAGSCILGNITIGEAKIGSGSVVVKDVPARTAVGNPARLIGKE 287	
Db 225 CGDRHKIGDGVLIGAGATLGNITRIGAGKVGAGSVVVLIDVPCTRGAVGNPARLIGKE 284	
QY 288 NPKHD-KPCLMDOTSYTEWSDVI 314	
Db 285 KPTIHD-EFGESMDHTSFISEWSDYII 312	

RP	SEQUENCE FROM N.A.	Oy	80 LESALAHILSVKLSNLNPNTLELFISVLEBESPEIESTKQDLIAVKERDPACTSYVH 139
RC	STRAIN=CV. COLUMBIA;	Db	113 LEQALGFVLANRLNQPTLQLDIFGVMMDKGQSSIRHDQAFKDRPACLSY 172
RA	"Howard J.R., Roberts M.A., Wray J.L.;	Qy	140 CFLGFKFLACQAHRIAHILWKONRKIVALLIONRVSEFAVDIHPGAKIGGILDHAT 199
RT	Arabidopsis thaliana.;"	Db	173 AILHLKGYHALQAVKAHKWNERKLLALQSRISVFIDHPARIGEGILDHGT 232
RT	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.	Qy	200 GWVIGETAVGDNVSLILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 259
RL	EMBL; AFL1203; AAD1963.1; -.	Db	233 GWVIGETAVGNGVSILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 292
DR	InterPro: IPR001451; -.	Qy	260 GSGSVWVKDVAPPATAVGNPARLICKEN----PRKHD 293
DR	Pfam: PF00132; hexapep; 2.	Db	293 AACSLVLDKVPSHSVVAGNPALKLIRVMEQDPSLAMKH 331
KW	transferase; Acetyltransferase.		
SQ	SEQUENCE 323 AA; 34534 MW; 8CE538962B44E610 CRC64;		
Query Match	Best Local Similarity 43.3%; Score 711; DB 10; Length 323;		
Matches	Local Similarity 50.5%; Pred. No. 7; e=50; Mismatches 78; Indels 12; Gaps 3;		
QY	27 FRPGFSVNRK-IHTQIEDD----DDWIKMELEEKSDVKQEPILSNYYASITSHRS 79	Qy	80 LESALAHILSVKLSNLNPNTLELFISVLEBESPEIESTKQDLIAVKERDPACTSYVH 139
Db	8 FESGEFVYAKGTHKSEEDSNLDPRSSPIWAIREEK-LEKEPTISFLYAGILAHDC 65	Db	113 LEQALGFVLANRLNQPTLQLDIFGVMMDKGQSSIRHDQAFKDRPACLSY 172
Qy	80 LESALAHILSVKLSNLNPNTLELFISVLEBESPEIESTKQDLIAVKERDPACTSYVH 139	Qy	140 CFLGFKFLACQAHRIAHILWKONRKIVALLIONRVSEFAVDIHPGAKIGGILDHAT 199
Db	68 LEQALGFVLANRLNQPTLQLDIFGVMMDKGQSSIRHDQAFKDRPACLSY 127	Db	173 AILHLKGYHALQAVKAHKWNERKLLALQSRISVFIDHPARIGEGILDHGT 232
Qy	140 CFLGFKFLACQAHRIAHILWKONRKIVALLIONRVSEFAVDIHPGAKIGGILDHAT 199	Qy	200 GWVIGETAVGDNVSLILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 259
Db	128 ATLHLKGYHALQAVKAHKWNERKLLALQSRISVFIDHPGAKIGGILDHGT 187	Db	233 GWVIGETAVGNGVSILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 292
Qy	200 GWVIGETAVGDNVSLILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 259	Qy	260 GSGSVWVKDVAPPATAVGNPARLICKEN----PRKHD 293
Db	188 GWVIGETAVGNGVSILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 247	Db	293 AACSLVLDKVPSHSVVAGNPALKLIRVMEQDPSLAMKH 331
Qy	260 GSGSVWVKDVAPPATAVGNPARLICKEN----PRKHD 293	Qy	80 LESALAHILSVKLSNLNPNTLELFISVLEBESPEIESTKQDLIAVKERDPACTSYVH 139
Db	248 AAAGSLVLDKVPSHSVVAGNPALKLIRVMEQDPSLAMKH 286	Db	113 LEQALGFVLANRLNQPTLQLDIFGVMMDKGQSSIRHDQAFKDRPACLSY 172
RESULT	11	RESULT	12
Q9S9B0	PRELIMINARY;	Q9SEY6	PRELIMINARY;
AC	PRT; 368 AA.	ID	Q9SEY6 PRT; 315 AA.
Q9S9B0;	05/10/2000 (Created)	DT	01-MAY-2000 (Tremblel. 13, Last sequence update)
DT	01-MAY-2000 (Tremblel. 13, Last sequence update)	DE	PUTATIVE SERINE ACETYLTRANSFERASE.
DT	01-JUN-2000 (Tremblel. 14, Last annotation update)	GN	Arabidopsis thaliana (Mouse-ear cress). Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; core eudicots; Rosidae; eurosids II; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis; OC
OK	NCBI_TaxID=3702;	OC	Brassicaceae; Arabidopsis; OC
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RC	STRAIN=CV. COLUMBIA;
RK	MEDLINE=20083487; PubMed=10617197;	RA	Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., RA
RK	NCBI_TaxID=3702;	RA	Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V., RA
RK	Nature 402:761-768(1999).	RA	Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., RA
RK	DR: AF024504; AF18673; 1;	RA	Cronin L.A., Shen M., Vankan S.E., Umayam L., Tallon L.J., Gill J.E., RA
DR	InterPro: IPR001451; -.	RA	Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., RA
DR	Pfam: PF00132; hexapep; 2.	RA	Copenhagen G.P., Preuss D., Nieman W.C., White O., Eisen J.A., RA
DR	PROSITE: PS00101; HEAPEPTRANSFERASES; 1.	RA	Salzberg S.L., Fraser C.M., Venter J.C.,
DR	KW Transferase.	RA	"sequence and analysis of chromosome II of Arabidopsis thaliana.;"
SQ	SEQUENCE 315 AA; 34000 MW; FD15AC3E8A150B2F CRC64;	RT	Nature 402:761-768(1999).
Query Match	Best Local Similarity 42.6%; Score 699; DB 10; Length 315;	Qy	27 FRPGFSVNRK-IHTQIEDD----DDWIKMELEEKSDVKQEPILSNYYASITSHRS 79
Matches	Local Similarity 50%; Pred. No. 7; e=49; Mismatches 76; Indels 14; Gaps 4;	Db	8 FESGEFVYAKGTHKSEEDSNLDPRSSPIWAIREEK-LEKEPTISFLYAGILAHDC 65
Qy	80 LESALAHILSVKLSNLNPNTLELFISVLEBESPEIESTKQDLIAVKERDPACTSYVH 139	Qy	80 LESALAHILSVKLSNLNPNTLELFISVLEBESPEIESTKQDLIAVKERDPACTSYVH 139
Db	66 LEQALGFVLANRLNQPTLQLDIFGVMMDKGQSSIRHDQAFKDRPACLSY 125	Db	140 CFLGFKFLACQAHRIAHILWKONRKIVALLIONRVSEFAVDIHPGAKIGGILDHAT 199
Qy	140 CFLGFKFLACQAHRIAHILWKONRKIVALLIONRVSEFAVDIHPGAKIGGILDHAT 199	Qy	126 AILHLKGYHALQAVKAHKWNERKLLALQSRISVFIDHPARIGEGILDHGT 185
Db	126 AILHLKGYHALQAVKAHKWNERKLLALQSRISVFIDHPARIGEGILDHGT 185	Qy	200 GWVIGETAVGDNVSLILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 259
Qy	200 GWVIGETAVGNGVSILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 245	Db	186 GWVIGETAVGNGVSILHGVTLGIGKQSGDRHKIGCVLIGASLTGNITIGGAKI 245
Db	53 FESGEFVYAKGTHKSEEDSNLDPRSSPIWAIREEK-LEKEPTISFLYAGILAHDC 112		

Db	246	AAGSLVLUKDVPSSHVVAGNPAKLIRYME-----EODPSLAM	281
RESULT	13		
ID	Q9JR86	PRELIMINARY;	PRT; 272 AA.
AC	Q9JR86;		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DE	CYTOSERINE ACETYLTRANSFERASE (EC 2.3.1.30).		
OS	Neisseria meningitidis (serogroup A), and		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=65699, 491;		
RN	[1] SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;		
RX	MEDLINE=2022256; PubMed=10761919;		
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,		
RA	Kliee S.R., Morell G., Basham D., Brown D., Chillingworth T., Hamlin N., Holroyd S.,		
RA	Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,		
RA	Jagels K., Leather S., Moulle S., Mungall K., Quail M.A.,		
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,		
RA	Whitehead S., Spratt B.G., Barrell B.G.;		
RT	"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";		
RL	Nature 404:502-506(2000).		
RN	[2] SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MC58 / SEROGROUP B;		
RX	MEDLINE=20175755; PubMed=10710307;		
RA	Tettelin H., Saunders N.J., Heidelberg J.J., Jeffries A.C., Nelson K.E.,		
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,		
RA	Nelson W.C., Gwynn M.L., DeBoy R.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,		
RA	Mason T., Ciecko A., Parsley D.S., Blair E., Cittone H., Clark E.B.,		
RA	Cotton M.D., Utterback T.R., Khouri H., Qin H., Vaithyanathan J., Gill J., Scarlato V., Magignani V., Pizza M., Grandi G., Sun L.,		
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappoli R., Venter J.C.,		
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain MC58";		
RL	Science 287:1809-1815(2000).		
DR	EMBL; ALI62754; CAB84026; -;		
DR	EMBL; AE00412; AAF40988; -;		
DR	TIGR; NMB560; -;		
DR	InterPro; IPR01451; -;		
DR	Pfam; PF00132; hexapep; 3.		
DR	Prosite; PS00101; HEXAPEP_TRANSFERASES; 1.		
KW	Transferase; PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.		
SQ	SEQUENCE 273 AA; 29278 MW; 5CBE16376B45B76F CRC64;		
Query Match	39.5%; Score 647.5; DB 2; Length 273;		
Best local Similarity	50.0%; Pred No 8.7e-45;		
Matches	132; Conservative 50; Mismatches 71; Indels 11; Gaps		
QY	39 HTQIEDDDWIKMEEKNSDKVQEPILSNVYYASITSHRSLESALAHLSVULKSLNLP 98		
Db	6 HTK-----WQDIAVEAREAOEQEPMLASFYHATIIKHDSDLAASLYTLANRINTASMP 59		
QY	99 SNTLFELPFISVLEESPETESTRKQDLIAVKERDPACISYVHCLFLGKGFLAQCAHRTAHT 158		
Db	60 AMAVRVEIEFAADPSISEAACDICATVNRDPAVSMSMLPLKYHALOGYRYAW 119		
QY	159 LDKRNKRKVALLIONYRESFADFVHIGAKIGKGILDHANGWVIGSTAVWDNVSTHG 218		
Db	120 IWKQQLRQKAYLQFQNNISVACQDNPDIHAPARIGRGMILDHATGVIGTAVWDVSIQD 179		
QY	219 VLGCTGKQSGDRHKPKGDVGLGAGSCSLGNITIGECAKIGSGSVVWDPARTAVGN 278		
Db	180 VLGCTGKQSGDRHKPKGDVGLGAGSCSLGNITIGECAKIGSGSVVLDQPARTAVGN 239		
QY	279 PARLGKENPRKHDKICPLCTMDQ 302		
Db	240 PARIVGRPQS---DK-PSLDMQ 258		
RESULT	15		
OSLZ8			
ID	Q9SLZ8	PRELIMINARY;	PRT; 402 AA.
AC	Q9SLZ8;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SERINE ACETYLTRANSFERASE.
 GN CMSAI.
 OS Cyanidioschyzon merolae.
 OC Elkaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.
 OX NCBI_TAXID=45157;
 RN [1]
 RX SQUENCE FROM N A.
 RP MEDLINE=98288115; PubMed=9622597;
 RA Toda K., Takano H., Miyagishima S., Kuroiwa H., Kuroiwa T.;
 RT "Characterization of a chloroplast isoform of serine acetyltransferase
 from the thermo-acidophilic red alga Cyanidioschyzon merolae.";
 RL Biochim. Biophys. Acta 1403:72-84(1998).
 DR EMBL: AB008428; BAA8412.1;
 KW Transf erase.
 SQ SEQUENCE 402 AA; 43739 MW; D97E69E8FF79F452 CRC64;

Query Match 38.4%; Score 629.5; DB 10; Length 402;
 Best Local Similarity 47.1%; Pred. No. 4 3e-43; Gaps 2;
 Matches 130; Conservative 51; Mismatches 92; Indels 3;

QY	DB	Sequence	
27	FGPGEFSVNRKIHHTQLEDDDWIKMLEAKRSDVQEPILSNVYVASYI	SHRSLESALAH 86	
97	FGPVISVDDMV-RTLTAVSSDPWELVRREAEIAGAANEPALOSSLYATVNHRCLEDTLAF	155	
QY	87	IILSVKLNLNLPNSNTEELFLSIVLEESPELETESTKODLIAVKERPACISYHCFLGFKG	146
	156	HIANELASPFQFATQVKLFRDALYDKDSYKREAIRADLLAVVRPPAMKICVAVIMYSKG	215
QY	147	FLACQAHRIAHTLWKONRKTVALLIONRVESFAVDIHPGAKIGKIGLILDHATGVVGET	206
Db	216	YAALQAYRLAHLWLRQDRKVLALEOSEISKCFAYDIPARIGSGVMIDHATGVVGET	275
QY	207	AVVGDANYSILRGVTLGGTGKGSQDRPKIGVGLIGAGSCITGNITIGEAKIGSGSVW	266
Db	276	AVVGNDVSMLNHNVTLGGTGKERAQDRHKPVGRGVVLGAGATVIGNIRGDQAQINASSVVL	335
QY	267	KYPARTTAVGPNRLLGKKNPRKDIPQLMDQ	302
	336	KYVPYPTIVSGVAPREVKLSYPK--GVYPAFEMDQ	369

Search completed: August 21, 2001, 12:10:05
 Job time: 182 sec